

#3

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/509,472

CRF Edit Date: 10-7-04  
Edited by: RL

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

**ENTERED**

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: ☒ invalid beginning/end-of-file text ; ☐ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

## RAW SEQUENCE LISTING

DATE: 10/07/2004

PATENT APPLICATION: US/10/509,472

TIME: 10:37:57

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10072004\J509472.raw

3 <110> APPLICANT: University of Utah Research Foundation  
 5 <120> TITLE OF INVENTION: ELASTIN PREVENTS OCCLUSION OF BODY VESSELS BY VASCULAR  
 SMOOTH  
 6 MUSCLE CELLS  
 8 <130> FILE REFERENCE: HYDR-PWO-005  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,472  
 C--> 11 <141> CURRENT FILING DATE: 2004-09-27  
 13 <150> PRIOR APPLICATION NUMBER: 60/368084  
 14 <151> PRIOR FILING DATE: 2002-03-27  
 16 <160> NUMBER OF SEQ ID NOS: 6  
 18 <170> SOFTWARE: PatentIn version 3.2  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2260  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1  
 26 ctcgagaaga gagggctcca gctccccaca gtagcccttg ccttcctctt tcccaggcag 60  
 28 gcggaggcac gcagatatac cattgacttc cctcccttg cagcaggcac atcctgggca 120  
 30 tcgagcttca gacctgccc ctgagcagcc cctaacccca ccaacaaagg gtggcttggg 180  
 32 ggggctttca cccagcata atctccatca gctaccctca aagcaccccc aaataaacac 240  
 34 acaccgtaag taagagctgt acactggctg tgtgcgtaca tcttcaagac aattctccca 300  
 36 gcatgcccct accttccaaa attccagagc tgctccctcc aaagaccagc ggaaaaggaa 360  
 38 gggtttgtcc agggctcctgg ggtggccccc tatagaccaa agcctgataa ctgtcctaga 420  
 40 agcagagtac ttgcagagcg agtgacggca actgtggtat tgacaccagt cctagcacca 480  
 42 gctgaacaca gagcattttt gatctagcag aaatacaaga ccacgttgta tttgtctttg 540  
 44 caataatctc ttagctagga atactgatca cctgtagaca gataaggaaa ctgatgctct 600  
 46 gtggagaggt tttcctacca gaaaggctag agccagaaat ttacttctag gtccaccaat 660  
 48 acctgccttt gaccaatgcc tgcatttgac ctttccacgc tgagccaccc ctgctggcac 720  
 50 tccagactgc cacagtgtc ctgcctccac aaggggctct taactcatcc ctggagcca 780  
 52 tcgtggtgca gggaaaagcc cacagggcgt gtggcttcca tgctgttccc tgactggctg 840  
 54 tgacctagga caaggaacaa gtttccctct cctattctct aggtctcaca tttcttctcc 900  
 56 tctagcagta gtgggaagtg aggggtgggg gacacgaccc tcccctgttc catccacac 960  
 58 tccaaccccc aaaatcccc aggggtcccc tccagctcag tcttgggggc agaaatgcag 1020  
 60 agttctccag gaacgtggtc ccagctgttt cagtgcaggc cgtccctctc tggccaccag 1080  
 62 cggaatgtca gccttcccag aggggcccgg agaacagcag tcgagaagct ccagactgg 1140  
 64 tgtgggcgct agctgtgtc agcgtgggga tgggaggtga ccagtgata atgggaagct 1200  
 66 gggctgcctg tcagtctgtg gggggctccc acctccctgt tccccacag ggcacctggg 1260  
 68 gatccagcct gatttttacc agacctgcgg cctgcatggg gctgggtata gggctgtgac 1320  
 70 cttgacctat gcagaataga acctgtgtg tggggtacct ccatgtgtc cagatgcccc 1380  
 72 tggggacagc accaaccatgg ccttaactcc caagccattc cctgcctct aacccctgg 1440  
 74 catctgcagg catccacccc agacccaccc aacacctct cccagcttc aggcgctagg 1500  
 76 cagagacctt ggccccctgca gaatgcagcc ctgtccaggg tcccctacct tccccccaga 1560  
 78 tccctcccag agcaatacca acccgggcct accttccagg ccattcaacc tgcagccccc 1620  
 80 cggcctctgt agacatcgca cccccaaac cccagacct gcccaatgcc tcccctcccc 1680

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82 agctttggggc agaacctgtc tctagccaga cctgggggtg ttggggagtc tggaggggccg 1740
84 ggggtgggggc tgaggcgcgg gacagctggc ccgtatcctc aactggggcc cagccggagg 1800
86 ggcggggggcc tggccactcg ggccttggct ggggctggga tttttggcct ggccgccagg 1860
88 cctcccttc tgcctcctct cccgagggtc gtccctggcag agggcccccct cgctctttct 1920
90 ggcgggaaca gggccagcag cgaaagaaca gtcgcagagg gaaagcggga aagagatggg 1980
92 ggaaagtgtg tgtgtgtgag tgtgtgcttg tgtgcatgtg tgtgcgtgtg ttgtgtcaag 2040
94 aaaaaagctc gcagtccagc agcccggggc tgggaggett gtgagccggg cctttcgtaa 2100
96 ttgtcccttc ccccgggccc cctccccag gcctcccccc tctcccgccc tcccggccgc 2160
98 cctctctccc tccctctttc cctcacagcc gacgaggcaa caattaggct ttggggataa 2220
100 aacgaggtgc ggagagcggg ctggggcatt tctccccgag 2260
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 757
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 2
110 Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Pro Gly Val Leu Leu Leu
111 1 5 10 15
114 Leu Leu Ser Ile Leu His Pro Ser Arg Pro Gly Gly Val Pro Gly Ala
115 20 25 30
118 Ile Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly Ala Gly Leu
119 35 40 45
122 Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro Gly Gly Lys Pro Leu Lys
123 50 55 60
126 Pro Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala Gly Leu Gly
127 65 70 75 80
130 Ala Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro Gly Gly Val
131 85 90 95
134 Ala Asp Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu
135 100 105 110
138 Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val
139 115 120 125
142 Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val
143 130 135 140
146 Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala Arg Phe
147 145 150 155 160
150 Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys
151 165 170 175
154 Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val
155 180 185 190
158 Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile
159 195 200 205
162 Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly
163 210 215 220
166 Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly
167 225 230 235 240
170 Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala
171 245 250 255
174 Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly
175 260 265 270

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Input Set : A:\pto.kd.txt

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```

178 Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala
179          275          280          285
182 Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala
183      290          295          300
186 Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala
187 305          310          315          320
190 Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val
191          325          330          335
194 Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro
195          340          345          350
198 Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val
199          355          360          365
202 Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly
203      370          375          380
206 Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly
207 385          390          395          400
210 Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly
211          405          410          415
214 Val Ala Gly Val Pro Ser Val Gly Gly Val Pro Gly Val Gly Val
215          420          425          430
218 Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Lys
219          435          440          445
222 Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala Ala Ala Ala Lys Ala
223      450          455          460
226 Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala
227 465          470          475          480
230 Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
231          485          490          495
234 Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly
235          500          505          510
238 Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala
239          515          520          525
242 Lys Ser Ala Ala Lys Val Ala Lys Ala Gln Leu Arg Ala Ala Ala
243      530          535          540
246 Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro
247 545          550          555          560
250 Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly
251          565          570          575
254 Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu
255          580          585          590
258 Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro
259          595          600          605
262 Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys
263      610          615          620
266 Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly
267 625          630          635          640
270 Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro
271          645          650          655
274 Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe

```

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```

275          660          665          670
278 Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu
279          675          680          685
282 Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala
283          690          695          700
286 Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly
287 705          710          715          720
290 Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe
291          725          730          735
294 Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys
295          740          745          750
298 Gly Arg Lys Arg Lys
299          755
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 6
304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: A bioactive fragment of tropoelastin.
310 <400> SEQUENCE: 3
312 Val Gly Val Ala Pro Gly
313 1          5
316 <210> SEQ ID NO: 4
317 <211> LENGTH: 6
318 <212> TYPE: PRT
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Control random fragment.
324 <400> SEQUENCE: 4
326 Val Ser Leu Ser Pro Gly
327 1          5
331 <210> SEQ ID NO: 5
332 <211> LENGTH: 582
333 <212> TYPE: DNA
334 <213> ORGANISM: Homo sapiens
336 <400> SEQUENCE: 5
337 atggctgcc a tccggaagaa actggtgatt gttggtgatg gagcctgtgg aaagacatgc      60
339 ttgctcatag tcttcagcaa ggaccagttc ccagaggtgt atgtgccac agtgtttgag      120
341 aactatgtgg cagatatcga ggtggatgga aagcaggtag agttggcttt gtgggacaca      180
343 gctgggcagg aagattatga tcgcctgagg cccctctcct acccagatac cgatgttata      240
345 ctgatgtgtt tttccatcga cagccctgat agtttagaaa acatcccaga aaagtggacc      300
347 ccagaagtca agcatttctg tcccaacgtg cccatcatcc tggttgggaa taagaaggat      360
349 cttcggaatg atgagcacac aaggcgggag ctagccaaga tgaagcagga gccggtgaaa      420
351 cctgaagaag gcagagatat ggcaaacagg attggcgctt ttgggtacat ggagtgttca      480
353 gcaaagacca aagatggagt gagagagggt tttgaaatgg ctacgagagc tgctctgcaa      540
355 gctagacgtg ggaagaaaaa atctggttgc cttgtcttgc ga      582
358 <210> SEQ ID NO: 6
359 <211> LENGTH: 193
360 <212> TYPE: PRT

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Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10072004\J509472.raw

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361 <213> ORGANISM: Homo sapiens
363 <400> SEQUENCE: 6
365 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys
366 1 5 10 15
369 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu
370 20 25 30
373 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu Val
374 35 40 45
377 Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu
378 50 55 60
381 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile
382 65 70 75 80
385 Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro
386 85 90 95
389 Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile
390 100 105 110
393 Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu His Thr Arg
394 115 120 125
397 Arg Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Glu Glu Gly
398 130 135 140
401 Arg Asp Met Ala Asn Arg Ile Gly Ala Phe Gly Tyr Met Glu Cys Ser
402 145 150 155 160
405 Ala Lys Thr Lys Asp Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg
406 165 170 175
409 Ala Ala Leu Gln Ala Arg Arg Gly Lys Lys Lys Ser Gly Cys Leu Val
410 180 185 190
413 Leu

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/509,472

DATE: 10/07/2004

TIME: 10:37:58

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10072004\J509472.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date